



QY	PD000001; Euk_1 kinase;	1.
SMART:	SM00194; RING;	1.
DR	SMART; SM00220; S_TK_C; 1.	
PROSITE:	PS0107; PROTEIN_KINASE_ATP; 1.	
DR	PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.	
PROSITE:	PS00518; ZF_RING_-1; FALSE_NEG.	
DR	PROSITE; PS00089; ZF_RING_-2; 1.	
KW	Transferase; Serine/threonine-protein kinase; ATP-binding; Phosphorylation; Zinc-finger.	
NON_CRF	1	
FTN_FING	424	473 RING-TYPE.
FTN_DOMAIN	1226	1491 PROTEIN KINASE.
FTN_DOMAIN	403	412 POLY-SER.
FTN_DOMAIN	925	932 POLY-THR.
FTN_DOMAIN	1165	1170 POLY-GLU.
NP_BIND	1232	1239 ATP (BY SIMILARITY).
BINDING	1245	1255 ATP (BY SIMILARITY).
ACT_SITE	1352	1352 BY SIMILARITY.
SEQUENCE	1495 AA;	163653 MW; 2D6ECB5217AFC4B CRO64;
SO		
Query Match	96.0%	Score 7515; DB 1; Length 1495;
Best Local Similarity	97.8%	Pred. No. 1.2e-308;
Matches 1461; Conservative	3;	Mismatches 28; Indels 2; Gaps 2;
QY	21 SPEAGGGGALKASSAPAAAAGLIREAEGSGGRERADWRRQLRKVRSVYELDQLEQPQFL 80	
Db	2 SPEAGGGGALKASSARAAAAGLIREAEGSGGRERADWRRQLRKVRSVYELDQLEQPQFL 61	
QY	81 AASPPASSTSPSPPADAGSGTGQFQPTAVPPPHGAARRGGAHTEVAAPDSGASSPA 140	
Db	62 AASPPASSTSPSPPADAGSGTGQFQPTAVPPPHGAARRGGAHTEVAAPDSGASSPA 121	
Qy	141 AEPGEKRAAAEPSSPAAPAGREMENKEITLGKHHKMDRPEERMIREYKLAKTOMPAWHE 200	
Db	122 AEPGEKRAAAEPSSPAAPAGREMENKEITLGKHHKMDRPEERMIREYKLAKTOMPAWHE 181	
Qy	201 WLERRNRGPVVVKPIPKYRGDGSEMMHLLAESPGEVQASAASAPASKGRRSPGNSPGR 260	
Db	182 WLERRNRGPVVVKPIPKYRGDSMNMHLLAESPGEVQASAASAPASKGRRSPGNSPGR 241	
Qy	261 TVKSESPGTRKRKVSPVFFQSGRTTPPRAPSPDGFSPPSYSPPEETNRRNKVMBARYLQ 320	
Db	242 TVKSESPGTRKRKVSPVFFQSGRTTPPRAPSPDGFSPPSYSPPEETNRRNKVMBARYLQ 301	
Qy	321 QIGPNFLIGGSDDNKRYFVIGQNCSCARGTCIHLFVMERVFOLEPSDPMLWRKT 380	
Db	302 QIGPNFLIGGSDDNKRYFVIGQNCSCAHGTCIHLFVMLRVFOLEPSDPMLWRKT 361	
Qy	381 KNEFEVSLFQKYHSRRSRKAPSRNTIQKFVSRMSNHTLSSSTSSENNSIKDEE 440	
Db	362 KNEFEVSLFQKYHSRRSRKAPSRNTIQKFVSRMSNHTLSSSTSSENNSIKDEE 421	
Qy	441 QMCPTCLGMLDEEFLTYCEDGCRNKHLHHCMSTWAECRRNREPLTCRKEKWRSHDF 500	
Db	422 QMCPTCLGMLDEEFLTYCEDGCRNKHLHHCMSTWAECRRNREPLTCRKEKWRSHDF 481	
QY	501 YSHLSSPPDSSPSSLLRAQQOTYQQPLAGSRRRNQESFNLTGYTQOIPPAYKDLAPW 560	
Db	482 YSHLSSPPDSSPSSLLRAQQOTYQQPLAGSRRRNQESFNLTGYTQOIPPAYKDLAPW 541	
Qy	561 IQVFGMELVGCLFSRNWNVRMAILRLSHDVSGALLANGESTGNSSGSSGSSPGGTS 620	
Db	542 IQVFGMELVGCLFSRNWNVRMAILRLSHDVSGALLANGESTGNSSGSSGSSPGGTS 601	
Qy	621 GSSTOSISSDVYACCSVLSMVCADPVKYYAALKTRAMLYTTPCHSLAERTKQLRLL 680	
Db	602 GSSQTISSEDVVECCSIVLMSVCADPVKYYAALKTRAMLYTTPCHSLAERTKQLRLL 661	
Qy	681 QPYVDITLVKCADANSRTSOLSTISTLLELKQGAELAGVRETLKAGSSTGIGGYDVNLNC 740	
Db	662 QPYVDITLVKCADANSRTSOLSTISTLLELKQGAELAGVRETLKAGSSTGIGGYDVNLNC 721	
RESULT	2	
M3K_MOUSE	ID M3K1_MOUSE STANDARD; PRT; 1493 AA.	
AC	P53149; Q60831; Q9R0U3; 01-OCT-1996 (Rel. 34, Created)	
DT	16-OCT-2001 (Rel. 40, Last sequence update)	
DT	15-JUN-2002 (Rel. 41, Last annotation update)	
DE	Mitogen-activated protein kinase kinase 1 (MEKK kinase) (MAPK/ERK kinase 1) (MEK kinase).	
GN	Map3k1 or MEKK1 or MEKK.	
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.	
NCBI_TAXID	=10090; [1]	
RN	SEQUENCE FROM N.A.	
RP	Lange C.A., Blumer K.J., Sather S.L., Johnson G.L.; Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.	
RL	[2]	
RN	SEQUENCE OF 1-659 FROM N.A.	
RP		

RC TISSUE="Spleen"; PubMed=10523642;  
 RX MEDLINE=9945510; PubMed=10523642;  
 RA Ito M.; Yoshioka K.; Arai M.; Yamashita S.; Takamatsu N.;  
 RA Sugiyama K.; Hibi M.; Nakabeppe Y.; Shiba T.; Yamamoto K.-I.;  
 RT "JSAP1, a novel Jun N-terminal protein kinase (JNK) binding protein  
 that functions as a scaffold factor in the JNK signaling pathway.";  
 RT Mol. Cell. Biol. 19:7539-7548(1999).  
 RN [3].  
 RP SEQUENCE OF 660-1493 FROM N\_A.  
 STRAIN=BAB/C; TISSUE=Heart;  
 RA Whitmarsh A.J.; Shore P.; Sharrocks A.D.; Davis R.J.;  
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.  
 CC FUNCTION: CAN PHOSPHORYLATE AND ACTIVATE MAPKK 1 AND MAPKK 2  
 (MEK1/MEK2) WHICH LEADS TO PHOSPHORYLATION OF MAP KINASES.  
 CC POTENTIALLY ACTIVATES THE JNK/SAK GROUP OF MAP KINASES.  
 CC TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE HEART AND SPLEEN WHILE  
 CC A LOWER LEVEL EXPRESSION IS SPEN IN THE LIVER.  
 CC -1- AUTOPHOSPHORYLATED.  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC -1- MAP KINASE KINASE SUBFAMILY.  
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.

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CC EMBL; AF117340; AAD5049.1;  
 DR EMBL; BAA14614; BAA5878.1;  
 DR EMBL; L13103; AAA97300.1; ALT\_INIT.  
 DR EMBL; U23470; AAA85038.1; -.  
 DR DR; Q0054; 1B71.  
 DR MGI; MGI:1346872; Map3k1.  
 DR InterPro; IPR000719; Euk\_pkinase.  
 DR InterPro; IPR004290; Ser\_Thr\_Pkinase.  
 DR InterPro; IPR001245; Tyr\_Pkinase.  
 DR InterPro; IPR001841; Znf\_finger.  
 DR ProDom; PF00069; pkinase; 1.  
 SMART; SM00184; RING\_1.  
 SMART; SM00219; TYRK\_1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS50010; PROTEIN\_KINASE\_ST; 1.  
 DR PROSITE; PS50051; ZF\_RING\_1; FALSE\_NEG.  
 DR PROSITE; PS50089; ZF\_RING\_2; 1.  
 KW Transferase; Serine/threonine\_protein\_kinase; ATP-binding;  
 KW phosphorylation; Zinc-finger.  
 FT ZN\_FING 438 487 RING-TYPE.  
 FT DOMAIN 1224 1489 PROTEIN\_KINASE.  
 FT DOMAIN 25 32 POLY-GLY.  
 FT DOMAIN 74 149 PRO-RICH.  
 FT DOMAIN 233 291 PRO-RICH.  
 FT DOMAIN 417 426 POLY-SER.  
 FT NP\_BIND 1230 1237 ATP (BY SIMILARITY).  
 FT BINDING 1253 1253 ATP (BY SIMILARITY).  
 FT ACT\_SITE 1350 1350 BY SIMILARITY.  
 FT CONFLICT 30 39 GGGALQSGA -> ALQSGG (IN REF. 2).  
 FT CONFLICT 103 103 MISSING (IN REF. 2).  
 FT CONFLICT 257 257 V -> E (IN REF. 2).

FT CONFLICT 307 307 M -> V (IN REF. 2).  
 FT CONFLICT 413 413 S -> C (IN REF. 2).  
 FT CONFLICT 559 559 V -> A (IN REF. 2).  
 FT CONFLICT 883 883 V -> L (IN REF. 3).  
 FT CONFLICT 1467 1467 V -> L (IN REF. 3).  
 SQ SEQUENCE 1493 AA; 161288 MW; CA5C9B7703CBF9 CRC64;

Query Match 88.4%; Score 6920.5; DB 1; Length 1493;  
 Best Local Similarity 89.5%; Pred. No 1 1e-283;  
 Matches 1360; Conservative 46; Mismatches 81; Indels 31; Gaps 11;

QY 1 MAAAAGNRASSSSGFPGARATSPAA--GGGGGAIKASSAPAA-AAGLLRAGSGGRERAD 56  
 DB 1 MAAAAGDRASSSSGFPGAAASPEAGGGGGALOSGAPAGAAGLRLFGSAERAD 60

QY 57 WRRQLRKVRSYELDQLPQPFL-AASPPASSTSPEADAAGSGTGQPVAYPPHG 115  
 DB 61 WRRQLRKVRSYELDQLPQPFLAAASPCTSPSPEADAAGASRQPAAGPPPG 120

QY 116 AASRGGAHLTESVAAPDSGASSPAAAEPGERAPAAEPSPAAAPACREMENKETLKGHK 175  
 DB 121 AASRCGSHSAELAARSGARPAGAEP-----PS-AAAPSREMENKETLKGHK 170

QY 176 MDDRPDEERMIREKLXKATCPMPKXHEWLERNRGRGPVVVKLPIVKGDSEMMHAAESPGE 235  
 DB 171 MEDRPEERMIREKLXKATCPMPKXHEWLERNRGRGPVVVKLPIVKGDSEVNLAAPQGE 230

QY 236 YOASAASPAASKGRSPSPGNPSGRATYKESSEPVGRKRKSPVPPFQSGRITPPRASPQG 295  
 DB 231 GQGSAAPKGRRSPSPGSSPSGRSPGKSPVGRKSPVFPQSGRITPPRASPQG 290

QY 296 FSYSPEPSTNRRYNKYNNRARLYLQQGPNSELIGGSPDNDKRYFQGPQNSCARTEFC 355  
 DB 291 FSYSPEPSTSRYYNKYNNRARLYLQQGPNSELIGGSPDNDKRYFQGPQNSCGRGAFC 350

QY 356 IHLFVMLRVFQLEPSPDPMILWKT1KAEFEVESLFOKYHSRSRSRRIKAPSRTNTIQEVSRM 415  
 DB 351 IHLIFVMIRVFOLEPSPDMILWKT1KAEFEVESLFOKYHSRSRSRRIKAPSRTNTIQEVSRM 410

QY 416 SNSHTLSSSTSSSENNSIKDDEEQNCPCICLGMIDEEQSLTCEDGCRLKLHHCMISW 475  
 DB 411 SNSHTLSSSTSSSENNSIKDDEEQNCPCICLGMIDEEQSLTCEDGCRLKLHHCMISW 470

QY 476 AEECRRNREPLICPLCRSKWRSHDYFSEISSLSDVDPSSLSRAQQQTIVQQPLAGS\_RRN 534  
 DB 471 AEECRRNREPLICPLCRSKWRSHDYFSEISSLSPVSEASLRVQQPSPQPVAGSORN 530

QY 535 QESNENIHYGTQIPPKYDIAEPWIQFCMBLVGCCFISRWNNVREMDAQLRLSHDVSGA 594  
 DB 531 QESSNLTHTGTQIPPKYDIAEPWIQFCMBLVGCCFISRWNNVREMDAQLRLSHDVSGA 590

QY 595 LLANGESTGNGGSSGSSPSGGATSGSSQTSISGDYVEACCVSLNVCADPVKYVVA 654  
 DB 591 LLANGESTGNGGSSGSSPSGGATSGSSQTSISGDYVEACCVSLNVCADPVKYVVA 650

QY 655 LKTRAMLYTPCHSLAFRIKYLQPVDTIILVKCADANSRTSOLISITSLLELCGQA 714  
 DB 651 LKTRAMLYTPCHSLAFRIKYLQPVDTIILVKCADANSRTSOLISITSLLELCGQA 710

QY 715 GELAVGRETLKASIGGQDYQINCLGNOTESNNNOELIGRCLDLLEPFAFY\_P 774  
 DB 711 GELAVGRETLKASIGGQDYQINCLGNOTESNNNOELIGRCLDLLEPFAFY\_P 770

QY 775 HIVSTDVSAAEPVIRYKKLSSLTFALOSIDNSHSMYGLSRRYISSLARVYTYPHV\_F 834  
 DB 771 HIVSTDVSQAEPVIRYKKLSSLTFALQSIDNSHSMYGLSRRYISSLARVYTAVF 830

QY 835 SKLDEMLSYSSSTTRMRFLRMLTADEVIEA1QLGVETLDQQDSFLQASVPNNY 894  
 DB 831 SKLYTMILNASGSTHTFRMRLLREVDTIILVKCADANSRTSOLISITSLLELCGQA 889

QY 895 ETENNNSPECTVHLEKTKGGLCATKLASSEDISERLASISVGPSSSSTTTTTEQK\_P 954

Db 890 ---BNSLLEHTVIREKTKGGLSATRLSASSESDSRLAGVSGLPSS----TTTEOPKP 941  
 QY 955 MYQTGKRPHSQCLNSSLPSHSQLMPALSTPSSSTPSVPGTATDYSKHLRQGFPCRI 1014  
 CC -|- PIM: AUTOPHOSPHORYLATED.  
 CC -|- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC -|- MAP KINASE KINASE SUBFAMILY.  
 Db 942 AVQTKGRPHSQCLNSSLPSH-HAQLMPEPAPSAPSAVP---DISKHREQAFLVCKI 995  
 CC -|- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.

Db 1015 PSASQTOPQRKFSLDFHRNPENPKSDKLSPVITOSRPLPSNNHHRPKPSRPPTPGNTSKQ 1074  
 QY 996 PSASQTOPQRKFSLDFHRNPENPKSDKLSPVITOSRPLPSNNHHRPKPSRPPTPGNTSKQ 1055  
 Db 1075 DPSSRNSMTLDLNSSSKCDDSFGC5CSNSNAV1SDEYVTPVEEKCRLDVNTELNSSTD 1134  
 QY 1056 DASSMSMTLDLGSSRCDDSFGGGNSNAV1SDEYVTPVEEKCRLDVNTELNSSTD 1115  
 Db 1135 LLEAMPSSDTTVFKSEAVLSEPEKAENDDTYKDDYHNNQCKEMAEEEAALAMA 1194  
 QY 1116 LLEAMPSSDTTVFKSEAVLSEPEKAENDDTYKDDYHNNQCKEMAEEEAALAMA 1175  
 Db 1195 MSAODALPIVPOLOVENGDIITIQQDPETLFGHTKAKOPYREDATEWLKGQOIGLGA 1254  
 QY 1176 MSAODALPIVPOLOVENGDIITIQQDPETLFGHTKAKOPYREDATEWLKGQOIGLGA 1235  
 Db 1255 SSCYQADYGTGTLMKVKTYTNTTSSEQEVEYEALREEIRTMKHNHPNTTRMLGATC 1314  
 QY 1236 SSCYQADYGTGTLMKVKTYTNTTSSEQEVEYEALREEIRTMKHNHPNTTRMLGATC 1295  
 QY 1315 EKSYNNLFIEWMAGGSVAHLSKYGAFKESVYVNTYEQLRLGSLSYLHENQITHRDYKGAN 1374  
 Db 1296 EKSYNNLFIEWMAGGSVAHLSKYGAFKESVYVNTYEQLRLGSLSYLHENQITHRDYKGAN 1355  
 QY 1375 LLIDSTGQRRIADGAAARLASKCTGAREFOGLLTIAFMAREFLVRLQQYGRSCDWS 1434  
 Db 1356 LLIDSTGQRRIADGAAARLASKCTGAREFOGLLTIAFMAREFLVRLQQYGRSCDWS 1415  
 QY 1435 VGCATEMAAKPNAEKAHSNHALIFKTAATATAPSIPSHLSPGLDVALROLELQPO 1494  
 Db 1416 VGCATEMAAKPNAEKAHSNHALIFKTAATATAPSIPSHLSPGLDVALROLELQPO 1475  
 QY 1495 DRPPSRELLKHPVFRWTW 1512  
 Db 1476 DRPPSRELLKHPVFRWTW 1493

RESULT 3  
 M3K1\_RAT ID M3K1\_RAT STANDARD; PRT; 1493 AA.  
 AC 062925; DT 01-NOV-1997 (Rel. 35, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DE Mitogen-activated protein kinase kinase 1 (MEK kinase 1) (MEKK 1).  
 DE (MAPK/ERK kinase 1 OR MEKK).  
 OS Rattus norvegicus (Rat).  
 OC Metacercaria; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine; Rattus  
 OX NCBI\_TaxID:10116;  
 RN SEQUENCE FROM N.A., AND MUTAGENESIS.  
 RC TISSUE; Brain;  
 RX MEDLINE=962244276; PubMed=8643568;  
 RA Xu S., Robbins D. J., Christerson L. B., English J. M.,  
 RA "Cloning of rat MEK kinase 1 cDNA reveals an endogenous membrane-  
 associated 195-kDa protein with a large regulatory domain.",  
 RL Proc. Natl. Acad. Sci. U.S.A. 93:5201-5205(1996).  
 CC -|- FUNCTION: CAN PHOSPHORYLATE AND ACTIVATE MAPKK 1 AND MAPKK 2  
 (MEKK1/MEKK2) WHICH LEADS TO PHOSPHORYLATION OF MAP KINASES. MOST  
 POTENTIALLY ACTIVATES THE JNK/SAPK GROUP OF MAP KINASES, AND LESS  
 EFFICIENTLY ERK2 OR P38.  
 CC -|- SUBCELLULAR LOCATION: MEMBRANE ASSOCIATED.  
 CC -|- TISSUE SPECIFICITY: MOST HIGHLY EXPRESSED IN SPLEEN, KIDNEY, AND  
 CC LONG.

CC -|- PIM: AUTOPHOSPHORYLATED.  
 CC -|- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC -|- MAP KINASE KINASE SUBFAMILY.  
 CC -|- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.

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CC EMBL; U48596; AAC525996.1;  
 CC HSSP; Q00534; 1B1T;  
 CC InterPro; IPR00719; Euk\_Pkinase.  
 CC InterPro; IPR002290; Ser\_thr\_Pkinase.  
 CC InterPro; IPR01841; Znf\_fing.  
 CC Pfam; PF00059; Pkinase\_1;  
 CC Prodrom; PD000001; Euk\_Pkinase; 1.  
 CC SMART; SMC0184; RING\_1;  
 CC SM00220; S\_TKC\_1;  
 CC PROSITE; PS00101; PROTEIN\_KINASE\_ATP; 1.  
 CC PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.  
 CC PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 CC PROSITE; PS00518; ZF\_RING\_1; FALSE\_NEG.  
 CC PROSITE; PS00089; ZF\_RING\_2; 1.  
 CC KW Transferase; Serine/Threonine-protein kinase; ATP-binding;  
 CC KW Phosphorylation; Zinc-finger; Zinc-finger.  
 CC FT 2N\_FING 433 482 RING-TYPE.  
 CC FT DOMAIN 1224 1489 PROTEIN\_KINASE.  
 CC FT DOMAIN 25 29 POLY-GLY.  
 CC FT DOMAIN 74 149 PRO-RICH.  
 CC FT DOMAIN 233 291 PRO-RICH.  
 CC FT DOMAIN 412 421 POLY-SER.  
 CC FT DOMAIN 1163 1168 POLY-GLU.  
 CC FT BINDING 1230 1237 ATP (BY SIMILARITY).  
 CC FT BINDING 1253 1253 ATP (BY SIMILARITY).  
 CC FT ACT\_SITE 1350 1350 BY SIMILARITY.  
 CC FT MUTAGEN 1369 1369 D->A: INACTIVATION.  
 CC SQ SEQUENCE 1493 AA; 8C5F29F866898324 CRC64;

Query Match 88.1%; Score 6892.5 ; DB 1; Length 1493;  
 Best Local Similarity 89.2%; Pred. No. 1,7e-282;  
 Matches 1356; Conservative 45; Mismatches 96; Indels 23; Gaps 8;

Qy 1 MAAAAGNRASSSGFPGARATSPBAGGGGALKASSAPAAGAHLREAGSGGERADWRR 60  
 Db 1 MAAAAGDRASSSGFPGAAASPAAGGGALQSGAPAGGLRETSAGGERADWRRQ 60

Qy 61 QLKVRVSYELDQIPEQFLAASPAPPASSTSPSPEPADAAAGGSGTGFQPVAVVPHGAAASRG 120  
 Db 61 QLKVRVSYELDQIPEQFLAASPAPPATSPSPEPADAAAGGSGTGFQPVAVVPHGAAASRC 120

Qy 121 GAHUTESVAAPDGASSPAAEGERKAAEPSPAAAGREMENKETLKGHLKMDDRP 180  
 Db 121 GHSAELAARDSCARSAPGAE-----FS-AAAPSGREMENKETLKGHLKMDDRP 170

Qy 181 EERNIREKLIKATCPAWKHWLERRNRGPVYKIPYKGDSMEMNLAAESPGEVQASA 240  
 Db 171 EERNIREKLIKATCPAWKHWLERRNRGPVYKIPYKGDSMEMNLAAELOQEGCAGS 230

Qy 241 ASPAKGRRSPSPNPSPTVSESPGTRKRVSPVQSGRITPPRAPSDFGFSY 300  
 Db 231 AAPAKGRRSPSPNPSPTVSESPGTRKRVSPVQSGRITPPRAPSDFGFSY 290

Qy 301 PEETNRRVRYKMRARLYLQQIGPNSELIGGSDPDKNYRFIGQNCSRCRGTCIBLLF 360  
 Db 291 PEETSRVVKYMRARLYLQQIGPNSELIGGSDPDKNYRFIGQNCSRCRGTCIBLLF 350

Qy 361 VMLRFQLEPSPDPMWLWRTKLKNFEVESLQKYHSRSSRRIKAPSRNTIQFYSRMSNSHT 420  
 Db 351 VMLRFQLEPSPDPMWLWRTKLKNFEVESLQKYHSRSSRRIKAPSRNTIQFYSRMSNSHT 410



DR EMBL; D10389; BAA01226; 1; -  
 DR X61227; CAA12788; 1; -  
 DR EMBL; X77923; CAA54896; 1; -  
 DR EMBL; Z43370; CAA83389; 1; -  
 DR EMBL; M83604; CAA83388; 1; -  
 DR PIR; S20117; S20117; AAA21179; 1;  
 DR PIR; S2285; S2285;  
 DR PIR; JQ1118; JQ1118;  
 DR PIR; JQ1432; JQ1432;  
 DR HSSP; P2941; ICKP;  
 SGD; S000631; BCK1;  
 InterPro; IPR000719; Euk\_Pkinase;  
 DR InterPro; IPR002290; Ser\_thr\_Pkinase;  
 DR Pfam; PF00065; Pkinase; 1.  
 DR Prodom; PD00001; Bck1\_Pkinase; 1.  
 SMART; SM00220; S\_TKc; 1.  
 PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.  
 KW Transferase; Serine/threonine-protein kinase; Tyrosine-protein kinase;  
 ATP-binding; Phosphorylation; DOMAIN; 1.175  
 FT DOMAIN; 1.440  
 NP\_BIND; 1.189  
 FT BINDING; 1.204  
 FT ACT\_SITE; 1.204  
 BY SIMILARITY.  
 FT ACT\_SITE; 1.303  
 PHOSPHORYLATION (BY PKC) (POTENTIAL).  
 FT MOD\_RES; 1.134  
 T -> P (IN BCK1-19; ACTIVATION).  
 FT VARIANT; 1.119  
 I -> T (IN BCK1-11; ACTIVATION).  
 FT VARIANT; 1.120  
 I -> V (IN BCK1-16; ACTIVATION).  
 FT VARIANT; 1.120  
 G -> V (IN BCK1-10; ACTIVATION).  
 FT VARIANT; 1.146  
 A -> P (IN BCK1-20; ACTIVATION).  
 FT VARIANT; 1.174  
 A -> P (IN BCK1-20; ACTIVATION).  
 FT CONFLICT; 59  
 F -> I (IN REF. 3).  
 FT CONFLICT; 79  
 E -> V (IN REF. 2).  
 FT CONFLICT; 264  
 A -> P (IN REF. 3).  
 FT CONFLICT; 279  
 N -> I (IN REF. 3).  
 FT CONFLICT; 703  
 RYPTDPSYYDR -> STPKPRVITME (IN REF. 3).  
 FT CONFLICT; 795  
 S -> A (IN REF. 3).  
 FT CONFLICT; 802  
 L -> V (IN REF. 3).  
 FT CONFLICT; 808  
 A -> S (IN REF. ).  
 FT CONFLICT; 903  
 T -> N (IN REF. 3).  
 FT CONFLICT; 919  
 A -> P (IN REF. 3).  
 FT CONFLICT; 960  
 ADA -> RDR (IN REF. 5).  
 FT CONFLICT; 1086  
 RYPPDPSYYEFIQLGNGK -> VPIAHTTSSYRMDLTVKNN  
 H (IN REF. 5).  
 SEQ SEQUENCE; 1478 AA; 164194 MW; DS86C3A497A5BB33 CRC64;

Query Match 7.9%; Score 619; DB 1; Length 1478;  
 Best Local Similarity 21.0%; Pred. No. 5.2e-19; Gaps 64;

Matches 332; Conservative 232; Mismatches 552; Indels 466;

QY 224 ENNHLAAESPGEYQASAASPASKR-----RSPPSG-----NSPGSRTVKSESPGVRKKR 273  
 DB 24 KFHQPTSSVASTKSSSKSPRTSKRYIIDDTSQPNLTPNSTSSQFYES-----74

QY 274 VSEVPFQSGRTPRRAFPSPDPSPEETNRVNKVMARLYLQQIGPNSFLGGDS 333  
 DB 75 -TIVIEQSFNWT-----TDDHISAGGLE-----NPTSTFNNSYK 107

QY 334 PDNKYRPIFGPQNCSCAR----GTCIHLFLMRYFQLEPSDPLW---RKT-----379

DB 108 NDN-----GPSSLSDRKSSGNSNSLSEDFKLILSWDPDDENTMHRTSWFKEHDF 161

QY 380 -----LNKFEEVBSLFQKYHSRSSRRIKAPSRTNIKFVSR-MSNS 413  
 DB 162 PESWLFKKHQLEFGHREFIKLLAYDNFAVYERYLPQTKTASYTRFQOLLKRTMTKNTNS 221

QY 419 H-----TLSSSSSTSSSEN1RDBEQMPCIPICLGMDEBLSLTVCEDGC---RNK 466

DB 222 HIROKASAKLKSRSRSESSISIKSNKNSQOE-DISNSRSTSSESALSPTKSGPSKTDEKNF 280

QY 467 LHHCMSIWAECRRNREPLICLCSRSHDFYSHLSSPVDSPLSLRAAQQTVOQQ 526

Db 281 IH-----STSTHDKTKSASSLYRRSFSLRGSSSSNASSAKSPSNKL---SIPAR 328  
 Qy 527 PLAGSRNQESNFNLHYGQIIPRAYKDLAEPWIQVGFNMELVGCLFERSNNVREMALLR 585  
 Db 329 P----HSIENSTLTKSASSPAPSPYS-----IFRRI-----HR 360  
 Qy 587 LSHDVSSLALLANGESTGNSGSSGSSPSSGATSSS-----QTSISGDVYEAACS 637  
 Db 361 SSSSESSULNSLFGSGIGEEAPT -ENPOGISLSSSENLAKGSKSHYETNVSPLQOS--- 416  
 Qy 638 VLSIMVCAVPVYKVVALKTRIAMLVTPCISLAERIKLQLLPPVVDTIVLKCADANSR 697  
 Db 417 -SLPTDDKGNUW---NKFERKSQGYPSPNTVAVTSQ-----ETPLK---SNSS 461  
 Qy 698 TSQLSISPL-----LELRGQAGBLAYERLAKTAGSIGGVDVYLNCILGN 744  
 Db 462 TATLVQTADVNIPSPSSSPPIKTAWSLEVISPDTPKISSTTASFKETYPDCINPD 521  
 Qy 745 OT--ESNNWQELLGRCLIDRLLEPFAEFYPHYISTDVSOAE-----PV 787  
 Db 522 KTPVVPYN-QKYSVKNFNLDDQ-----KFTP-LKTKGLNDSENKYILVTKDNYSFVPL 572  
 Qy 788 EIR-YKKLSSLTFALOSIDSNSHSMV-----GK 814  
 Db 573 NLASVAKUSSFKESALAKLGJNHKNVTFHMTDFCDIGAA1PDDTLEFLKSLFLNTSGK 632  
 Qy 815 LSRRILSSARMVTTVPHFVKLEMVLSSSSTHTMRRIUMADEVETAEAIQ---LG 872  
 Db 633 TYIKDMKLOQPKPAPLITSENNVPLSKVSKSSMRSGTSSJIASTDVSVTSSSDITS 692  
 Qy 873 VEDTLGQODSFLOATSPVNNYLETTENSSP-----ECTVHLEKTGKGLCAT---KL 920  
 Qy 693 EDEHASGSGRYRQ---TFSYYYDVRVSNTNPTEELNWNKIEVLSHEENAPKVMVFKTSPLK 750  
 Db 793 RESPYTKPLA-PKREAKKPANTSPTQRLSTSQKNPKIRVLRASTKLSR-----842  
 Qy 921 SASSEDISERLASISVGSSSTTTTTEQPKEPVQYTKGRPHSQCLNSS---PLSHH 975  
 Qy 1034 PENKDSDKLSPVFTQSPRPLPSNTHRP-KPSRTPGNTSKQGDPSKNSMTH-----D 1084  
 Db 751 ELNLPDGSKL-----NIPPTENESKSSEQVLRKDEGEIDEFNHR 792  
 Qy 976 SOLMF--PALSTPSSTSPVSPAGTATDVSKHRLQGFTPCRIPSASPTOKRKSQFLHRNC 1033  
 FT CONFLICT; 59  
 FT CONFLICT; 79  
 FT CONFLICT; 264  
 FT CONFLICT; 279  
 FT CONFLICT; 703  
 FT CONFLICT; 795  
 FT CONFLICT; 802  
 FT CONFLICT; 808  
 FT CONFLICT; 903  
 FT CONFLICT; 919  
 FT CONFLICT; 962  
 FT CONFLICT; 1086  
 FT CONFLICT; 1104  
 H (IN REF. 5).  
 SQ SEQUENCE; 1478 AA; 164194 MW; DS86C3A497A5BB33 CRC64;

Qy 1085 LNSSSKCD-DSFGCOS-----NSSNAVIPSDETVP---TP-----VEEKCRL 1122  
 Db 890 VMRRLKTDQOISSTSPSLRMQKVNRNSNSTVSNSNISFYSPSPJLKKRGNNSKRVSSTSAA 949

Qy 1123 DVNTBLNSSEEDLLEASMP-----SSDTTVFKSEVAV-----LSPEAEN 1163  
 Db 950 DIFEE-----NDITFADAPPMFDSDDDSSSSDDIIWSSKTTAPEINNRKDERSDN 1004  
 Qy 1164 DDTYKDDVNHNQKKEKEM-----AEEPEALAIAMMASASODA 1201  
 Db 1005 SSTHSDEIFYDSDQCDKMERKMTTRPSPEVYQNLKEKPRANLDKPTEGIASPTSPKS 1064  
 Qy 1202 L-----PIVQLOVE-----NGEDIYLIQODTP-----1224  
 Db 1065 LDSLLSPKVNAYASSRTEPSTPSRYPDPSSEYFIDGLNGKPKLNQATPKRTKTIRTIA 1124  
 Qy 1225 -----ETLPGH---TRAKQPREDTE-WLKGQQIGIG 1252  
 Db 1125 HEASLARKNSVNLKRONTKWGTTRMVEVNEMYSINKNSKGEYKEFWMGEMIGKG 1184  
 Qy 1253 AFSSCYQADQYGTGTLMAKQVTYVRNTSSEQEY---VEALREBTRMNSHLNHPNTRM 1309  
 Db 1185 SFAYVILCLAVTTGEMAVQVE -VPKYSQNEALSLTVEALREVSFLKDLBLHNTVOY 1243  
 Qy 1310 LGATECKSNYNLFIEMAGGSVAHLLSKYGAFKESVINYTEQLLRLGSYLHENQITHR 1369  
 Db 1244 LGFENRNNIYSLFLBVAGGSVGSIRMYGRFDEPLKHITQVLKGLAYLHSKGJLHRD 1303

Qy	1370	VKGANLIDSTGQRLLTADFGAAARLASKRGTAGEFOGLIGTIAFMPEVLRGQQ-YGR	1428
Db	1304	MKDNLNLDDQDG-ICKISDFGSRK- SKDITSN-S-DMTMRGTVFENMAPEWYDTKQGYSA	1359
Oy	1429	SCDYWSVGCAIIEMACAKPPWAEKHSNHLIFKIASATTPAPSIPSHLSPGLRDVALR-	1487
Db	1360	KVDIWLGCIVLEMFKRKPWS--NLEVVAAFMFKICKSKSAPPIDTLPLISQICRNF	1416
Qy	1488	--CLEYLOPQDRPSRELLKHP	1506
Db	1417	LDAGEEINEPEKRPTANELLSHP	1438
RESULT 5			
	M3K3_MOUSE	M3K3_MOUSE	STANDARD;
ID	Q61084;	PRT;	626 AA.
AC			
DT	01-NOV-1997 (Rel. 35, Created)		
DT	01-NOV-1997 (Rel. 35, Last sequence update)		
DT	30-MAY-2000 (Rel. 39, Last annotation update)		
DE	Mitogen-activated protein kinase kinase 3 (EC 2.7.1.-)		
DE	(MAPK/ERK kinase kinase 3) (MEKK 3) (MEK kinase 3) (MEKK 3).		
GN	MAP3K3 OR MEEK3.		
OS	OS mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
NCBI_TAXID	=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Brain;		
RX	MEDLINE-96214986; PubMed-8621389;		
RN	Blank J.L., Gewins P., Elliott E.M., Sather S., Johnson G.L.;		
RT	"Molecular cloning of mitogen activated protein/ERK kinase kinases (MEKK) 2 and 3. Regulation of sequential phosphorylation pathways involving mitogen-activated protein kinase and c-Jun kinase.";		
RT	J. Biol. Chem. 271:5361-5368 (1996).		
RL			
CC	- FUNCTION: PREFERENTIALLY ACTIVATES P42/44 (ERK2/ERK1) MAP KINASES.		
CC	- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.		
CC	MAP KINASE KINASE SUBFAMILY.		
CC	-----		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation, the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <a href="http://www.isb-sib.ch/annou">http://www.isb-sib.ch/annou</a> or send an email to license@isb-sib.ch).		
CC	-----		
DR	U43187; AAB0335.1; -.		
DR	HSSP; Q00334; 1B18.		
DR	MGD; MGI:1346874; Map3k3.		
DR	InterPro; IPR000719; Ser_thr_Pkinase.		
DR	PFAM; PF00069; Pkinase; 1.		
DR	PRODOM; PD000001; Euk_pk kinase; 1.		
DR	SMART; SM00220; STC; 1.		
DR	PROSITE; PS000107; PROTEIN_KINASE_ATP; FALSE_NEG.		
DR	PROSITE; PS000108; PROTEIN_KINASE_ST; FALSE_NEG.		
DR	PROSITE; PS55011; PROTEIN_KINASE_DON; 1.		
KW	Transferase; Serine/threonine protein kinase; ATP binding.		
FT	DOMAIN 362 PROTEIN KINASE.		
FT	NP_BIND 368 ATP (BY SIMILARITY).		
FT	BINDING 391 391 ATP (BY SIMILARITY).		
FT	ACT_SITE 489 489 BY SIMILARITY.		
SEQUENCE	626 AA; 70775 MW; 00EF2442C9E56E0B CRC64;		
Query Match	7.1%; score 559; DB 1; Length 626;		
Best Local Similarity	29.9%; Pred. No. 6.4e-17;		
Matches	167; Conservative 87; Mismatches 188; Indels 116; Gaps		
Qy	1016 SASPOTORKESIQLQHRCNPENKDSKLSPVFTQSRLPSSN-----IHRKP-----		1062

Db	110	SSMSKSRILLSQDRN	--HTSSSPHSQVSQVRIPQSQSGDINTIYQAEPQRSTHLS	166
Qy	1063	--SRPTPG	--NTSKQGDPSPKSNSMTLDLNSSSRCDDSFQCSNSSNATP	110
Db	167	VSSQNPRGRSSPPGYYPERQHQIARQ-	--SYT-----SINSEGIFP	206
Qy	1108	SDETVFTPVVEICRDLNTELNSIEDILEAMPSDITVTKSEVAVLSP	--	115
Db	207	E-----TSEQMQLPLSSAENSLSQSCQSDRSANSPSTFKSOMBRARSPFDNRKECS	259	
Qy	1159	--EKAENDDTY-----KUDVNHNOKCKERMEAEELAII--AMAMSASQ	119	
Qy	260	DRETQYDGVKGRTGPRYHVSVHHDYNGDRTFPTRRQGGLNLFLVPSSRLSTING	319	
Qy	1200	DALPIVQ-----LQYENGEDILIIQDTPETLPGHTKAKOPPYREDETTEWLGKQQIGL	125	
Db	320	EUNGAVAYOQYDPLGRRLRSADSENALTYQERNYT-----KSP-SAPINWRKGKLGQG	371	
Qy	1253	APESSCYQAOQDVGTGLMKVQTYVNTISSEQEVVEAALREEIRMMSHLNHNNTIIRMGA	131	
Db	372	AFGRVLYCXDYDTGRELASKOYQFDPD-SPETSKVEASALECEIQLLNKLQHENIVQYGC	430	
Qy	1313	TCKNSN--YNLFTEWAGGSVAHLLSKYGAFKESVVINYTEQLLRLGSLYLHENQIHRDV	137	
Db	431	LRRRAEKLLTIPMEYMPGSSVKQDQKAYGALTESVTRYTQROLEGMESYLHSNMIVHBDI	490	
Qy	1371	KGANLIDSTGQRRIADEAARLAS---KGPGAGEFGQOLLGTTIAPEAVRQGQY	142	
Db	491	KGANLRSAG-NVKLDFGASKRQLOTICMSGIGI---RSVIGTPWMSPEVIGSEGYG	545	
Qy	1428	RSCDHWSSVGCAIIMACAKPPNAEKHSNHLALKIASATTATPSIPSHLSPGLRDVALR	144	
Db	546	RKDADWSLGCTVEMLTKEPPW-AEYEA--MAAFIKFIATQPTNFQLPISHSERGRDF-LR	601	
Qy	1488	CLEQPOQDRPPSREPLLKH	1505	
Db	602	RIPVBARQPSAEEELLTH	619	
<b>RESULT 6</b>				
M3K3_HUMAN	ID	M3K3_HUMAN	STANDARD;	PRT;
AC	Q99759;			626 AA.
DT	01-NOV-1997	(Rel. 35)	Created	
DT	01-NOV-1997	(Rel. 35)	Last sequence update	
DT	15-JUN-2002	(Rel. 41)	Last annotation update	
DE	Mitogen-activated protein kinase kinase 3 (EC 2.7.1.-)			
DE	(MAPK/ERK kinase 3) (MEK kinase 3) (MEKK 3).			
GN	MAPK3 OR MAPK3 OR MEKK3.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. MEDLINE=9116058; PubMed=9006902;			
RA	Ellinger-Ziegelbauer H.C., Brown K., Kelly K., Siebenlist U.;			
RT	"Direct activation of the stress-activated protein kinase (SAPK) and extracellular signal-regulated protein kinase (ERK) pathways by an inducible mitogen-activated protein kinase/ERK kinase kinase 3 (MEKK derivative);"			
RT	J. Biol. Chem. 272:2668-2674 (1997).			
CC	- FUNCTION: PREFERENTIALLY ACTIVATES P42/44 (ERK2/ERK1) MAP KINASE;			
CC	- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.			
CC	MAP KINASE KINASE SUBFAMILY.			
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CC kinase) (MAPKKK).  
DR BYR2 OR STB8 OR SPBC1D7.05.  
DR Schizosaccharomyces pombe (Fission yeast).  
DR Gene; HNC; 6555; MAP3K3.  
DR Genew; HNC; 6555; MAP3K3.  
DR MIM: 602339; -.  
DR Inter-Pro; IPR00719; Euk\_pkinase.  
DR InterPro; IPRO02290; Ser-thr\_pkinase.  
DR Pfam; PF00069; Pkinase\_1.  
DR Probom; PRO000001; Euk\_pkinase; 1.  
DR SMART; SM0220; S\_TRC; 1.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; FALSE\_NEG.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; FALSE\_NEG.  
DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
DR Transferase; Serine/threonine\_protein\_kinase; ATP-binding.  
KW DOMAIN 362 622 PROTEIN KINASE.  
FT NP\_BIND 368 375 ATP (BY SIMILARITY).  
FT BINDING 391 391 ATP (BY SIMILARITY).  
FT ACT\_SITE 489 489 BY SIMILARITY.  
SQ SEQUENCE 626 AA; 70969 MW; E0F11F5082EPA810 CRC64;

Query Match 7.1%; Score 558.5; DB 1; Length 626;  
Best Local Similarity 30.3%; Pred. No. 6.7e-17; Indels 101; Gaps 20;  
Matches 164; Conservative 85; Mismatches 191; RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=972;  
RX MEDLINE=21848401; PubMed=11859360;  
RA Wood V., Gwilliam R., Rajandream M.A., Lyne R., Lyne R., Stewart A.,  
RA Stourds J., Peat N., Hayles J., Baker S., Baslam D., Bowman S.,  
RA Brocks K., Brown D., Churcher C.M.,  
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,  
RA Gentles S., Goble A., Hamlin N., Harris D., Hodson G.,  
RA Holroyd S., Hornby T., Howarth S., Hidalgo J., Hunt J., Jagels K.,  
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,  
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odeil C.,  
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabbinowitsch E.,  
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,  
RA Shelton J., Simmonds M., Squares R., Squares S., Stevens K.,  
RA Taylor K., Taylor P.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,  
RA Woodward J., Volkerta G., Aert R., Robben J., Grynpont B.,  
RA Weltjens I., Vanstreels E., Riiger M., Schaefer M., Mueller Auer S.,  
RA Gabell C., Fuchs M., Fritze C., Holzer F., Moestl D., Hilbert H.,  
RA Borzym K., Langer T., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,  
RA Eger P., Zimmermann W., Wambutt R., Purnelle B.,  
RA Goftau A., Cadieu E., Dreano S., Glouz S., Lealaire V., Mottier S.,  
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Hurst S.M.,  
RA Lucas M., Rochelet M., Gailhard C., Garzon A., Thode G.,  
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Ray F., Benito J.,  
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,  
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen T., Potashkin J.,  
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;  
DB 277. RRYHYSVHHHDYSDQDRRTPRIRHQGNFLTYSSRSRSLTNGNMGIAVQYDPPRGLR 336  
QY 1170 -----DVNHNOQCKEKMEEEEEALI-----AMMASAQDALPIVQ-----LQ 1209  
DB 217. LSSAENSLSSCQSLDRAUDSPTRKSRSRQAQFDNQEYSLRETOLYDKGVKGTTYP 276  
QY 1129 NSSIDDLLEASMPSSDTTVY--TJKSEVAVLSPPEKAENDDTYKD-----1169  
DB 188. HIARGD----SYT-----SINSGEFPE----TSEQCMLDP----216  
QY 1069 NTISGQDPSSNSMTLNLSSSKCDSDFCGSSNSNAVPSDTEVFTPEEKCQLDNTYL 1128  
DB 1210 VENGEDLIIQDDEBTLEGHTKAKQPYRBDTEWIKQQIGLAFQASSCYQADYGTGIM 1269  
QY 1270 AVKQTYVVRNTSSEQEVYEAIRRMSHLNPNITMLGATEKSNYL--FIENMA 1327  
DB 389 ASKPKQFDDED-SPEKTSKEYSALEETQIOLKLNLOHERTYQYGCRRDAEKTLTTFMEMP 447  
DB 1388 DFGAAARLAS--KGTTGAGEFQQQLGTIAFMAPPVLRQGQQYGRSCDWVGAIIEAAC 1444  
QY 1328 GSVAHLLSKYGAFKRSVVNTYBOLLRLGSYHLHENQI1HRDYKGANLJIDSTQQRRLIA 1387  
DB 448 GGSVDRDQLKAYGALTESVTRKYTRQILEMSLYHSNMTHDQGANLIRDAG-NVKLG 506  
QY 507 DFGASKRLQTCMGTG---MRSTGTPXWMSSEVISGEYGEKADWLSLGCTVVELT 562  
QY 1445 ARKPPWAERKHSNHLALIFKIASATAPSTAPSLEQFQDRPPSRELIK 1504  
DB 563 EKPPWAEYEA-MAIFIKAQTQPNPQLSHISEHGRDE-LRKFVEARQPRAEELT 618  
QY 1505 H 1505 PRT; 659 AA.  
Db 619 H 619

RESULT 7  
BYR2\_SCPO ID BYR2\_SCPO STANDARD;  
ID BYR2\_SCPO STANDARD;  
AC P28829; 24, Created  
DT 01-DEC-1992 (Rel. 24, Last sequence update)  
DT 01-DEC-1992 (Rel. 24, Last annotation update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Protein kinase byr2 (EC 2.7.1.-) (protein kinase\_st8) (MAPK kinase

CC kinase) (MAPKKK).  
DR BYR2 OR STB8 OR SPBC1D7.05.  
DR Schizosaccharomyces pombe (Fission yeast).  
DR Gene; HNC; 6555; MAP3K3.  
DR Genew; HNC; 6555; MAP3K3.  
DR MIM: 602339; -.  
DR Inter-Pro; IPR00719; Euk\_pkinase.  
DR InterPro; IPRO02290; Ser-thr\_pkinase.  
DR Pfam; PF00069; Pkinase\_1.  
DR Probom; PRO000001; Euk\_pkinase; 1.  
DR SMART; SM0220; S\_TRC; 1.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; FALSE\_NEG.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; FALSE\_NEG.  
DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
DR Transferase; Serine/threonine\_protein\_kinase; ATP-binding.  
KW DOMAIN 362 622 PROTEIN KINASE.  
FT NP\_BIND 368 375 ATP (BY SIMILARITY).  
FT BINDING 391 391 ATP (BY SIMILARITY).  
FT ACT\_SITE 489 489 BY SIMILARITY.  
SQ SEQUENCE 626 AA; 70969 MW; E0F11F5082EPA810 CRC64;  
QY 1016 SASPOTQRFKSLQPHRNCPENKDKLSSVFVTOGRPLPSSNTHRKPKPSRPTQ-----1068  
DB 129 SSSPHEVSQRVRIKASQASGDINTIYQPPPEPKRSRHSVSS-QNPGRSSSPPPGCVPRQQ 187  
QY 1069 NTISGQDPSSNSMTLNLSSSKCDSDFCGSSNSNAVPSDTEVFTPEEKCQLDNTYL 1128  
DB 188 HIARGD----SYT-----SINSGEFPE----TSEQCMLDP----216  
QY 1129 NSSIDDLLEASMPSSDTTVY--TJKSEVAVLSPPEKAENDDTYKD-----1169  
DB 217. LSSAENSLSSCQSLDRAUDSPTRKSRSRQAQFDNQEYSLRETOLYDKGVKGTTYP 276  
QY 1170 -----DVNHNOQCKEKMEEEEEALI-----AMMASAQDALPIVQ-----LQ 1209  
DB 277. RRYHYSVHHHDYSDQDRRTPRIRHQGNFLTYSSRSRSLTNGNMGIAVQYDPPRGLR 336  
QY 1210 VENGEDLIIQDDEBTLEGHTKAKQPYRBDTEWIKQQIGLAFQASSCYQADYGTGIM 1269  
DB 337 SADSENALSQERNVYPT-----KSP-SAPINRQRKGKULQGAFGRYLCYDVTGREL 388  
QY 1270 AVKQTYVVRNTSSEQEVYEAIRRMSHLNPNITMLGATEKSNYL--FIENMA 1327  
DB 389 ASKPKQFDDED-SPEKTSKEYSALEETQIOLKLNLOHERTYQYGCRRDAEKTLTTFMEMP 447  
DB 1388 DFGAAARLAS--KGTTGAGEFQQQLGTIAFMAPPVLRQGQQYGRSCDWVGAIIEAAC 1444  
QY 1328 GSVAHLLSKYGAFKRSVVNTYBOLLRLGSYHLHENQI1HRDYKGANLJIDSTQQRRLIA 1387  
DB 448 GGSVDRDQLKAYGALTESVTRKYTRQILEMSLYHSNMTHDQGANLIRDAG-NVKLG 506  
QY 507 DFGASKRLQTCMGTG---MRSTGTPXWMSSEVISGEYGEKADWLSLGCTVVELT 562  
QY 1445 ARKPPWAERKHSNHLALIFKIASATAPSTAPSLEQFQDRPPSRELIK 1504  
DB 563 EKPPWAEYEA-MAIFIKAQTQPNPQLSHISEHGRDE-LRKFVEARQPRAEELT 618  
QY 1505 H 1505 PRT; 659 AA.  
Db 619 H 619

SEQUENCE FROM N.A.  
RX MEDLINE=91260799; PubMed=1435753;  
RA Wang Y., Xu H.P., Riggs M., Rodgers L., Wigler M.;  
RA "byr2, a Schizosaccharomyces pombe gene encoding a protein kinase capable of partial suppression of the rasi mutant phenotype." Mol. Cell. Biol. 11:3554-3563(1991).  
RN [1]  
RN SEQUENCE FROM N.A.  
RX MEDLINE=93062799; PubMed=11859360;  
RA Steyksdottir U., Egil R., Nielsen O.;  
RA "Functional conservation between Schizosaccharomyces pombe ste8 and Saccharomyces cerevisiae STE11 protein kinases in yeast signal transduction." Mol. Genet. 235:122-130(1992).  
RN [2]  
RN SEQUENCE FROM N.A.  
RX MEDLINE=21848401; PubMed=11859360;  
RA Wood V., Gwilliam R., Rajandream M.A., Lyne R., Lyne R., Stewart A.,  
RA Stourds J., Peat N., Hayles J., Baker S., Baslam D., Bowman S.,  
RA Brocks K., Brown D., Churcher C.M.,  
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,  
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RA Holroyd S., Hornby T., Howarth S., Huckle E.J., Hunt J., Jagels K.,  
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RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odeil C.,  
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RA Taylor K., Taylor P.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,  
RA Woodward J., Volkerta G., Aert R., Robben J., Grynpont B.,  
RA Weltjens I., Vanstreels E., Riiger M., Schaefer M., Mueller Auer S.,  
RA Gabell C., Fuchs M., Fritze C., Holzer F., Moestl D., Hilbert H.,  
RA Borzym K., Langer T., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,  
RA Eger P., Zimmermann W., Wambutt R., Purnelle B.,  
RA Goftau A., Cadieu E., Dreano S., Glouz S., Lealaire V., Mottier S.,  
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Hurst S.M.,  
RA Lucas M., Rochelet M., Gailhard C., Garzon A., Thode G.,  
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Ray F., Benito J.,  
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,  
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen T., Potashkin J.,  
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;  
DB 277. RRYHYSVHHHDYSDQDRRTPRIRHQGNFLTYSSRSRSLTNGNMGIAVQYDPPRGLR 336  
QY 1170 -----DVNHNOQCKEKMEEEEEALI-----AMMASAQDALPIVQ-----LQ 1209  
DB 217. LSSAENSLSSCQSLDRAUDSPTRKSRSRQAQFDNQEYSLRETOLYDKGVKGTTYP 276  
QY 1210 VENGEDLIIQDDEBTLEGHTKAKQPYRBDTEWIKQQIGLAFQASSCYQADYGTGIM 1269  
DB 337 SADSENALSQERNVYPT-----KSP-SAPINRQRKGKULQGAFGRYLCYDVTGREL 388  
QY 1270 AVKQTYVVRNTSSEQEVYEAIRRMSHLNPNITMLGATEKSNYL--FIENMA 1327  
DB 389 ASKPKQFDDED-SPEKTSKEYSALEETQIOLKLNLOHERTYQYGCRRDAEKTLTTFMEMP 447  
DB 1388 DFGAAARLAS--KGTTGAGEFQQQLGTIAFMAPPVLRQGQQYGRSCDWVGAIIEAAC 1444  
QY 1328 GSVAHLLSKYGAFKRSVVNTYBOLLRLGSYHLHENQI1HRDYKGANLJIDSTQQRRLIA 1387  
DB 448 GGSVDRDQLKAYGALTESVTRKYTRQILEMSLYHSNMTHDQGANLIRDAG-NVKLG 506  
QY 507 DFGASKRLQTCMGTG---MRSTGTPXWMSSEVISGEYGEKADWLSLGCTVVELT 562  
QY 1445 ARKPPWAERKHSNHLALIFKIASATAPSTAPSLEQFQDRPPSRELIK 1504  
DB 563 EKPPWAEYEA-MAIFIKAQTQPNPQLSHISEHGRDE-LRKFVEARQPRAEELT 618  
QY 1505 H 1505 PRT; 659 AA.  
Db 619 H 619

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RX MEDLINE=21848401; PubMed=11859360;  
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QY 1210 VENGEDLIIQDDEBTLEGHTKAKQPYRBDTEWIKQQIGLAFQASSCYQADYGTGIM 1269  
DB 337 SADSENALSQERNVYPT-----KSP-SAPINRQRKGKULQGAFGRYLCYDVTGREL 388  
QY 1270 AVKQTYVVRNTSSEQEVYEAIRRMSHLNPNITMLGATEKSNYL--FIENMA 1327  
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DB 1388 DFGAAARLAS--KGTTGAGEFQQQLGTIAFMAPPVLRQGQQYGRSCDWVGAIIEAAC 1444  
QY 1328 GSVAHLLSKYGAFKRSVVNTYBOLLRLGSYHLHENQI1HRDYKGANLJIDSTQQRRLIA 1387  
DB 448 GGSVDRDQLKAYGALTESVTRKYTRQILEMSLYHSNMTHDQGANLIRDAG-NVKLG 506  
QY 507 DFGASKRLQTCMGTG---MRSTGTPXWMSSEVISGEYGEKADWLSLGCTVVELT 562  
QY 1445 ARKPPWAERKHSNHLALIFKIASATAPSTAPSLEQFQDRPPSRELIK 1504  
DB 563 EKPPWAEYEA-MAIFIKAQTQPNPQLSHISEHGRDE-LRKFVEARQPRAEELT 618  
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DB 337 SADSENALSQERNVYPT-----KSP-SAPINRQRKGKULQGAFGRYLCYDVTGREL 388  
QY 1270 AVKQTYVVRNTSSEQEVYEAIRRMSHLNPNITMLGATEKSNYL--FIENMA 1327  
DB 389 ASKPKQFDDED-SPEKTSKEYSALEETQIOLKLNLOHERTYQYGCRRDAEKTLTTFMEMP 447  
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QY 1328 GSVAHLLSKYGAFKRSVVNTYBOLLRLGSYHLHENQI1HRDYKGANLJIDSTQQRRLIA 1387  
DB 448 GGSVDRDQLKAYGALTESVTRKYTRQILEMSLYHSNMTHDQGANLIRDAG-NVKLG 506  
QY 507 DFGASKRLQTCMGTG---MRSTGTPXWMSSEVISGEYGEKADWLSLGCTVVELT 562  
QY 1445 ARKPPWAERKHSNHLALIFKIASATAPSTAPSLEQFQDRPPSRELIK 1504  
DB 563 EKPPWAEYEA-MAIFIKAQTQPNPQLSHISEHGRDE-LRKFVEARQPRAEELT 618  
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QY 507 DFGASKRLQTCMGTG---MRSTGTPXWMSSEVISGEYGEKADWLSLGCTVVELT 562  
QY 1445 ARKPPWAERKHSNHLALIFKIASATAPSTAPSLEQFQDRPPSRELIK 1504  
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QY	1018	S--POTQRKFESLQFRHNCPCENKODKLSPVF-----TQSRLPLPSNTHRKPSRPT-P	1067
Db	238	QSYNDPNHQEE-----SDYDNPFEFKGKGTYPRYHVSYHQRNDGKTFPP	284
QY	1068	GNTSQGDPKSNTMFLDNSSKKCDDSFCCSSNSNAVIPSDETVFPEEKRLDVNT	1127
Db	285	RARRQG----NQLTPV SFSPIDHSLSSTSSSS-----IFPEYEDSRI--RR	327
QY	1128	LNSSTEDLLEASMPSSDTTYTFKSEAVYLSPERAKENDDTYKDDYNNHQCKERMEAEEE	1187
Db	328	RGSDID-----NPFLT-----VMDSIP-----	344
QY	1188	ALATANAMSAQSODALPIVQLQVNGEDIIIQODTPETLPGHTKAKQPYRDEDTENLKQG	1247
Db	345	-----PSRSP-----PSRSP-----RAPTWNPLKG	359
QY	1248	QIGLGAFSSCCYQAQDGYTGTLMAYKVQTYVRNTSEQEVVEALREETRAMSHLNHPNII	1307
Db	360	LIGQAFGRVLCYDTCRELAYQVQDPD-SPETSKVNALECEQOLLKNFLHERIV	418
QY	1308	RMLGATC---EKSINYNLTERMAGSYAHLLSKYGAFKESVINYTEQLRLGSLSTHEN	1363
Db	419	QYYG--CLRDPOEQTLTSIMEYNGS1KDQKAYGALTENGSTRKYTRQILEGVYHLHSN	476
QY	1364	LRHDVKGANLITSTGQRLRATAARASL-----KGTGAGEFGFOLGLTGIAFRAPEV	1420
Db	477	MILHRDIKGANLIRSTG-NVKLDGFQGASKRLQTICLSTG-----MKSVTGPYWMSPV	531
QY	1421	LRGOQYGRSCDWWSYGCA1IEMACKAQPNAEKHSNHIALIFKIASATTAPSISLUSPG	1480
Db	532	1SGQGVRKADIWSACTVEMLEKPP-AEFTA--MAAIKJIAQTPNPKLPPHVSYD	588
QY	1481	LRDVNLRCLELOPDRPSPRELLKH-----	1505
Db	589	TRDFD-LKRIVKEAKRPSABDLE-----	612

RESULT 9		ST11 YEAST		STANDARD;		PRT:		738 AA.	
ID	ST11 YEAST	ID	P23561;	DT	01-NOV-1991 (Rel. 20, Created)	DT	01-OCT-1996 (Rel. 34, Last sequence update)	DT	16-OCT-2001 (Rel. 40, Last annotation update)
AC		DE	Serine/threonine-protein kinase STE11	GN	STE11 OR YLR362W OR L8059.10.	OS	Saccharomyces cerevisiae (Baker's Yeast)	OC	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomyces; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX	NCBI_TaxID:4932;	RA	Rhodes N., Connell L., Errede B.,	RT	STE11 is a protein kinase required for cell-type-specific transcription and signal transduction in yeast. Genes Dev. 4:1862-1874(1990).	RL		RN	
RN	[1]	RP	SEQUENCE OF 22-738 FROM N.A.	RA	STRAIN=S28C / AB972;	RA	Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z.,	RA	
RP		RX	MEDLINE=91115076;	RA	Favello A., Fulton L., Gattung S., Greco T., Kirsten J.,	RA	Kucaba T., Hallsworth K., Hawkins J., Hillier L., Jier M.,	RA	
RX		RA	PubMed=2276621;	RA	Johnson D., Johnston L., Langston Y., Latrille P., Le T.,	RA	Mardis E., Menzies S., Miller N., Nhan M., Pauley A., Peleuso D.,	RA	
		RA		RA	Rifkin L., Riles L., Taich A., Trevors J., Vignat A., Wohlman P., Vaudin M., Wilson R.,	RA	Wilcox C., Wohlgemuth P., Cairns B.R., Ramer S.W., Korber K.D.,	RA	
		RP	SEQUENCE FROM N.A.	RA	Submitted (JAN 1995) to the EMBL/GenBank/DBJ databases.	RP	POSSIBLE FUNCTION.	RA	
		RP	STRAIN=S28C / AB972;	RA	PubMED=1628833;	RP	MEDLINE=92331935;	RA	
		RX		RA	Cairns B.R., Ramer S.W., Korber K.D.,	RT	Order of action of components in the yeast pheromone response	RA	
		RX		RA		RT		RA	

QY	1092	DGSFGCSSSSNAVAPIPDETVPVEEKCRDVTNLSSLEDLLEASMPSSDTTIVTFKS	1151	DR Pfam; PF00069; Pkinase; 1.
Db	353	----ILLKHSDAV--DMAILQGLDQ-----TRLSSLK-----DTI-----	381	DR ProDom; PD000001; Euk_kinase; 1.
QY	1152	EYAVLSPPKAENDDTYKDVHNQKCKERMAEEALAIAAMSASQDALPIVQLOVE	1211	DR SMART; SM00220; S_TKC; PROTEIN_KINASE_ATP; 1.
Db	382	KIPKLAIKRPPENDAIS----NQEELLSVEGEE-----DHDFF-----	417	DR PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.
QY	1212	NGDIIIIIQDQPETLPGHTAKAQPYREDTEWLKGQOIGLGFQAOQVGTTGTLMAV	1271	KW Transferase; Serine/threonine-protein kinase; ATP-binding.
QY	418	-QEDSDIV----SLP-TKATP---KWKAGCIGSOSFGSTYLGMAHGTBELLMAV	464	PROTEIN KINASE DOMAIN
QY	1272	KOYEIKNNNIGPTDNNKQANSDENNEQQEQQEKIEDVGASHPKTNQNITHRMVDALQH	524	FT DOMAIN
Db	465	-----SSEQEE-----YVEALRE	1293	FT N_PBLND
QY	1273	-----YI-----YI-----YI-----YI-----YI-----YI-----	1293	FT BINDING
Db	525	ENLKLKEHHENITTYGASQGGNNNIFLYVPGSVSSMNNNGPFEEELITNPTRQI	584	FT ACT_SITE
QY	1354	LRLGSLYLNHQITHRDKYKGANLILIDSTGQRLRADIAGAARLASKGTTGAEFQGQLLGTI	1413	FT SEQUENCE
Db	585	LIGVAYHKKNTHRDKGANLILID-K-CYKTDGEGTSKTSPLNKQKQ-RASIQGV	642	SQ 6 8%; Score 531; DB 1; Length 619;
QY	1414	AFLMAPEVLRGQDGGRSCDWDVSYGCALEMACKPNAEKAHSNHALIFKIASATAPS1	1473	Matches 168; Conservative 78; Mismatches 214; Gaps 24;
Db	643	FNSMSPEVKYKATTAKADIVSNGCVYIEMFIGKHP---PDESONQATIFKIGNTT-PEI	698	Query Match
QY	1474	PSHLSPGRLDVALRCLELQPQRDRPSRELLKHP	1506	Best Local Similarity 28.4%; Pred. No. 9.4e-16;
Db	699	PSWATSEGKNFRLRAFELDYQTRPSALELQHP	731	Matches 168; Conservative 78; Mismatches 214; Gaps 24;
RESULT 10				Query 944 TTTTTEQPKPMVQTKGRPHSQCLNSSPSHQSOLMFPLSTPSSSTPSPVAGTADYVK 1003
M3K2_MOUSE		STANDARD:	PRT:	Db 1244 STQATNLLEPSPSPED-----LNNTPLGAERKRLSVYGPNNRDRSSUPPPGYIPDILH 175
AC	061083;			QY 1004 H -RLQGFIFPCR----IPSASPOTQRKISKPLDKSLPQFQHNCNPBKNDKSLPQFQSRPLPSSN 1056
DT	01-NOV-1997	(Rel. 35, Created)		Db 176 QIARGNSFTF1NSEGEFFIPESMDQMLDPFLSL----SSPENSGSGSCPSSL----DSPLDGE 228
DT	01-NOV-1997	(Rel. 35, Last sequence update)		QY 1057 IHRKPSPRPPTPNQKQGDPSKSNMTLDLNSSKDDSFQCSS-----NS 1101
DT	30-MAY-2000	(Rel. 39, Last annotation update)		Db 229 Y -PKSRMP----RAQSYDPDNHQEFETDID -NPLFEKKFGKGCTYPRRYHVSYHQEYN 279
DE	Mitogen-activated protein kinase kinase kinase 2 (MEK 2).	(MAPK2 OR MEKK2).		QY 1102 SNAVAPSDETVYFTPYEEKCILDVTELNSSEIDLEAAMPSSDTTVTFSEAVLSPERA 1161
GN	Mus musculus (Mouse).			Db 280 GRKTFF----RAIRTGQTSFRSPY----SSPSTDLSSTSGSSVFTPE - 320
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			QY 1162 ENDITYKDYNHNQKCKEKMEEEEEALIAMAMSASQDALPIVQLQWENGEDLIICQ 1221
OC	Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.			Db 321 -----YDDSRIRR----GSPI-----333
OX	NCBI_TAXID=10090;			QY 1222 DTPE-TLPGHTKAKDQPYREDTEWLKGQOIGLGAPESSQYQDQVGTGTLMAVKQTYVRNT 1280
RN	SEQUENCE FROM N.A.			Db 334 DNPLTUVTDSSPPSPSPRATPNWRUGKLQGAFGRVLYCDVDTGRELAVKQYQF -NPE 392
RP				QY 1281 SSEQEEEVVAREEIRMASHLNHPATIRMGATC---EFSNYNLFIELMAGGSAHLL 1336
RC				Db 393 SPETSKENVALECEQLKNULHERVQYYG--CLRDPEKTLISTEMELSPGGTSKIDQIK 450
CC	- SIMILARITY: BELONGS TO THE JNK/SAPK GROUP OF MAP KINASES. PHOSPHORYLATES MEK1 OR JNK MAP KINASE IN VITRO.			QY 1337 KYGAFKRESVVINYTQOLLRGSLYHEHQITHRDKYGANLILIDSTGQRLRITADFGAAARLA 1396
CC	MAP KINASE KINASE SUBFAMILY.			Db 451 AYGALTENWTRKYTQILEPHYLHSNMVHARDKGANLIRDSTG-NIIGDFASKRQ 509
CC	SEQUENCE FROM N.A.			QY 1397 S ---KGTGAGEFOGQILTAFAPEVLRLQQYGRQQGRSCDWSVGCATIENACAKPWNAAK 1453
RC				Db 510 TICLSTGT ---MKSVTGTPWMSPEVISBGYGRKADWVACTVVENLTEKPKW-AEF 564
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to licensee@isb-sib.ch).			QY 1454 HSNHIALIFTKATASATAPSIPSHLSPGLDVAIROLEQPDQPPSREJLKH 1505
CC	CC	CC	CC	Db 565 EA---MAIFKIAQTQTPNKLPEPHSYDTRDF-LKRIFVAKLPSAEELLRH 613
CC	CC	CC	CC	RESULT 11
CC	CC	CC	CC	ID MKH1_SCHP0 STANDARD; PRT; 1116 AA.
CC	CC	CC	CC	AC Q10407;
CC	CC	CC	CC	DT 01-OCT-1996 (Rel. 34, Created)
CC	CC	CC	CC	DT 01-OCT-1996 (Rel. 34, Last sequence update)
CC	CC	CC	CC	DT 15-JUN-2002 (Rel. 41, Last annotation update)
CC	CC	CC	CC	DE MAP kinase kinase mkh1 (EC 2.7.1.-).
CC	CC	CC	CC	GN MKH1 OR SPAC1F3.02C.
CC	CC	CC	CC	OS Schizosaccharomyces pombe (Fission Yeast).
CC	CC	CC	CC	OC Schizosaccharomyces pombe; Ascomycota; Schizosaccharomyces.
DR	EMBL; AB03536.1;			OC Schizosaccharomyces.
DR	MGI_11345873; Map312.			OX NCB_1_TaxID=4896;
DR	InterPro; IPR000719; Euk_kinase.			
DR	InterPro; IPR002290; Ser_thr_pk kinase.			



SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND MUTAGENESIS OF LYS-1371.

PROTEIN: Fetal liver, and Skeletal muscle;  
RXNDBP ID: 305639;  
MEDLINE: 97419143; PubMed: 305639;  
RA: Takekawa M.; Posas F.; Saito H.;  
"A human homolog of the yeast ssk2/Ssk22 MAP kinase kinase kinases,  
MTK1, mediates stress-induced activation of the p38 and JNK  
pathways";  
RT: EXBIO J. 16;4973-4982(1997).

RN: SEQUENCE OF 68-1607 FROM N.A. (ISOFORM B).  
RC: TISSUE-Bone marrow;  
RX: MEDLINE:97191544; PubMed:9039502;

RA: Nagase T.; Seki N.; Ishikawa K.-I.; Ohira M.; Kawarabayasi Y.;  
Ohara O.; Tanaka A.; Kotani H.; Miyajima N.; Nomura N.;  
"Prediction of the coding sequences of unidentified human genes. VI.  
The coding sequences of 80 new genes (KIA0201-KIA0280) deduced by  
analysis of cDNA clones from cell line KG-1 and brain.",  
J. Mol. Biol. 312:1-39(1996).

-1- FUNCTION: ACTIVATES THE CSBP2, P38 AND JNK MAP PATHWAYS, BUT NOT

THE ERK PATHWAY. SPECIFICALLY PHOSPHORYLATES AND ACTIVATES MAP2K4

AND MAP2K6.

-1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: A (SHOWN HERE) AND B; ARE

PRODUCED BY ALTERNATIVE SPLICING AT HIGH LEVELS IN HEART, PLACENTA,

SKELETAL MUSCLE AND PANCREAS, AND AT LOWER LEVELS IN OTHER

TISSUES.

-1- DOMAIN: THE N-TERMINAL NON-CATALYTIC DOMAIN (1-606) CONTAINS AN

ESSENTIAL DOMAIN FOR THE DOMINANT-INHIBITORY EFFECT.

-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

MAP KINASE KINASE SUBFAMILY.

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DR: EMBL: AF002715; BAB68804.1; -.

DR: EMBL: D86968; BAA13204.1; -.

DR: HSSP: P24941; 1HCL; -.

DR: GeneID: 6856; NAP3K4.

DR: MIM: 602425; -.

DR: InterPro: IPR000719; Euk\_kinase.

DR: InterPro: IPR000290; Ser\_thr\_kinase.

DR: ProDom: PD000001; Euk\_kinase; 1.

DR: SMART: SM00220; S\_TKc; 1.

DR: PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.

DR: PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.

DR: PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.

KW: Transerase; Serine/threonine-protein kinase; ATP-binding;

KW: Alternative splicing;

ET: DOMAIN 4 7 POLY-ALA.

ET: DOMAIN 25 38 POLY-PRO.

ET: DOMAIN 1190 1201 PROTOIN KINASE.

ET: DOMAIN 1342 1600 ATP (BY SIMILARITY).

ET: NP\_BIND 1348 1355 ATP (BY SIMILARITY).

ET: BINDING 1371 1371 ATP (BY SIMILARITY).

ET: ACT\_SITE 1462 1462 BY SIMILARITY.

ET: VARPASIC 1175 1223 MISSING (IN ISOFORM B).

ET: MUTAGEN 1371 1371 K>R: LOSS OF ACTIVITY.

ET: CONFLICT 791 791 I -> R (IN REF. 2).

SQ: 1607 AA; 181550 MW; 24BC459773OB5287 CRC64;

Query Match 6.4%; Score 502.5; DB 1; Length 1607;

Best Local Similarity 19.7%; Pred. No. 4.5e-14;

Matches 288; Conservative 239; Mismatches 574; Indels 363; Gaps 59;

Score 502.5; DB 1; Length 1607;

Qy: 209 GPVVVKPIPVKGDGSEMMHIAAESPGEVQASAASPAKGRRSPGNSPGRTVKSRSPG 268

Db: 4244 WPFEIPSRSKNEPEEGDDIEGELEESS----DESEBEQ 465

Qy: 269 VRRKRVSPPFQSGRITPRAAPSPDGSPYSPPEETNRVNVKMRARLYLQQGPNSFL 328

Db: 466 ISDPV-----PERIQDNTDSFIQSRCISKK-----LERLESEDS 503

Qy: 329 IGGDSPDNKVRVFPQONOSCARTFCIHLLFYMVLRFQLEPSPDPMILMRKTLNKEYESL 388

Db: 504 LGWGPAD-----WSTEAG-FSRICLTSYRPFV-----DKALKQMGFLRL 542

Qy: 389 FQKTHS-----PRSSRIKAPSENTRIKPVSMSMNSFTLSSSSTSSTSSSE - NSIRDE 438

Db: 543 ILRLHLKLMDSLQRARIYLAIVKNDRPRVEFFSEPPDPMNGSDYVOLSLRTPPEEKCSAVWE 602

Qy: 439 BEQMCPCILLGMLD---TEBSLTVCEDGCRKNKLH - HHMSWIADEECRNREPPLICPL - 490

Db: 603 E-----LKAMDPSFEEAFLV - CRVLLNYTHECLKLRLQE - PAGEPLSLSIKQ 650

Qy: 491 ----CRSKWRS-----HDFYSHELSSPVDPSSPLRAAQQTYYQQQPLAGSRRRNQESNF 539

Db: 651 LVRECKEVLGGLMXXQYQMLQEVLEDIEKP-----DCNI 687

Qy: 540 NLTHYGTQIPPPAYKDLAEPWIOQV-----GMELYGCIFLSRNW-----ENAL 584

Db: 688 DAEFDLHKMIVYFYMRSQYQMLQPOASHSFLRNLLBEWNFTKETHYIGGEA 747

Qy: 585 RRLSHDVGALLANGESTGNGGSSGSPSGGATSGSOTSISDVEAACSVLSMVA 644

Db: 748 GKLFCDTAQMLKSTSFELRGQESCAEWTSADSSADEIIIRSVIE ----- ISRALK 802

Qy: 645 DPVKVYVAALKTLRMLVTPCHSLAERIKLQLQVPPVDTI ---LVKCADANSRTSQ 700

Db: 803 ELFHEARERASKALGFAKMLRKDLDEAEEFRSLAPYRDLVLSKQYQVQIPGLENLQ 862

Qy: 701 LSITSLBLCLRGQAGEIAVRLKLKGSIGIGVGD-----YVINCILGNQTES 746

Db: 863 MFVPTDIL-----AEKSIIQLQINNAA-----GKDCCSKDSDDVLDIAYLILKHSDRARD 912

Qy: 749 N ----NWOELLGRCLCIDRLLLEPAFYHIVSTDVSQAREPEVIRYKILSLTFLAQ 803

Db: 913 SEDSMWGTEAQ -----PVKVNPOVETVDTLRSQMDV-----NULLVWQ 951

Qy: 804 STDNSHSMVGKLSRRIYSSARMYTV-----PHVSKULEMLSVSSSTHETMRMRRL 856

Db: 952 S---AHUJ-----QRKAQSQLEGMLTCQEQTSSQPYTIAKALQQLK ----- 991

Qy: 857 MAIADEVEIAEIQLQGYEDTLGQDQDFSLQASVNPNEYLETTSPECTYHEKTG----- 912

Db: 992 -- NDALELCNRISNAI - DRDHMFTEFDAVDESVT1QOYTREAMOGYNFEEYH 1047

Qy: 913 KGLCATKUASSDEDISERLASTSVGPSSSTITTTTQPKPWVQTGKRPHSQCLNSPL 972

Db: 1048 KEYVRLMSGEFROKIGRYISPARKWNVYVTKCESGTRTRWATQFDLQIAEPAFI 1107

Qy: 973 SHISQOLMPALSTPSSTPSVPGATADVSKHRLQGFIPCRIPSASQPTQKFSLOFHRN 1032

Db: 1108 SALPDDDSLISLQALMNEIGHYG-----KPH-----SPVT--GLYLATHRN 1147

Qy: 1033 CPENKDSKLPSPVETQSPRPL-----PSSNIHREKRP-----SRPUPGNTSKQGDPSRN 1079

Db: 1148 SP-----RPMKVPCHRSDPPNHLIIPPEGFSTRSMPDSARSHGSPAA 1192

Qy: 1080 SMIDLNSSSSKCDDSGCGSSNSNAVIPSDEFVFTPEEKCRDLVNTELNSSTIEDLEAS 1139

Db: 1193 AAAANAVASRPSPSGG-----DSVLEKS-----ISSAHDTGRSS 1227

Qy: 1140 MPSSDTTVTFKSEVAV-----LSPEKAENDDTYK - DVHNHQKCKE - KMEAEFEAL 1189

Db: 1228 VPENDRLLASIAAEQFRSLSRHSPTERDEPAYPRGDSGSTRSMELRLTLISQSCKDTA 1287

Qy: 169 TLGGLKHMDDPPEERMIREKLTATCPAWHEWL --ERRNRR----- 208

Db: 370 SLQALQDYEKYAAKDFQDRYQALC-----WLNITKDLNQLRIMGTIVLGIKNLSDIG 423

QY 1190 AIAAMASASODALITPOLQVENSEDIIIQ -DTPTLPG -HTAKOPPREDTEWLK 1245  
 Db 1288 SKLGDEIAQKSRIEEFYRMRKNNLIGQVDTPSYDNMVGILR -- KVTFWQR 1344  
 QY 1246 GQQIGLGFSSCYQAQDVGTGTLMAVKOVTYVENTSSEQEVYEALETRAMSHLNHPN 1305  
 Db 1345 GNKIGEGQCKVYTISVDIGELNAMEKTRFQN --- DHKTTKETADELKFGTIRHN 1400  
 QY 1306 IIRMLGATECKSNYNLFIEWMAGGSVAHLSKYGAFKESVVNTTEQLRLGLSYLHENQI 1365  
 Db 1401 LYRVEGVELREEMYCFIMYCDBTLEE-VSRL-LQEVVIRLYSKQTIAINVLAERGI 1458  
 DR 1459 VHRDLGANLFLDTGORIADGMAPLASKG-TGANGEFQSLGILTAFMAPEVL --- 1421  
 QY 1366 IHRDYGANLFLDTGORIADGMAPLASKG-TGANGEFQSLGILTAFMAPEVL --- 1421  
 Db 1459 VHRDLGANLFLDTSGC-LIKLGDGCSCVLLKNNATQMPGEV -NLTGTAAYMAPEVTRA 1516  
 QY 1422 RGQDYGRSDCVWSYSGATTIEMACKAPPPWNAEKHSNHALLFKAISATAPSIPSHLSPGL 1481  
 Db 1517 KGEHQGRADIWLSLQVYVEMTSRWPHEYEH -NEQTMVKYMG -HKPPIPERLSPBG 1573  
 QY 1482 RDVALCRELQDOPDRPSRELLKH 1505  
 Db 1574 KDFLHSCLESDPKMRWTASQLDH 1597

**RESULT 13**  
 ID M3K4\_MOUSE STANDARD; PRT; 1597 AA.  
 AC 008648; 008649; 07\_0124;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DE Mitogen-activated protein kinase 4 (MEK kinase 4) (MEKK 4).  
 GN MAP3K4 OR MEKK4.  
 OS Mus musculus (Mouse).  
 OC Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.  
 OX NCBI\_TAXID=10090;  
 RN 1] SEQUENCE FROM N.A. (ISOFORMS A AND B).  
 RP TISSUE:Brain.  
 RC MEDLINE:97236778; PubMed:9079650;  
 RA Gershwin P., Blank J.L., Johnson G.L.;  
 RT "Cloning of a novel mitogen-activated protein kinase kinase kinase, MEKK4, that selectively regulates the c-Jun amino terminal kinase pathway".  
 RL J. Biol. Chem. 272:8288-8295 (1997).  
 RN [2]  
 SEQUENCE OF 363-1049 FROM N.A.  
 RP STRAIN=C57BL/6; TISSUE:ectoplacental cone;  
 RX MEDLINE:9742605; PubMed:926631;  
 RA Schweiher N., Valk P.J., DeJewel R., Cox R., Francis F.,  
 RA Meier-Ewert S., Lehrach H., Barlow D.P.;  
 RT "Characterization of the C3 YAC contig from proximal mouse chromosome 17 and analysis of allelic expression of genes flanking the imprinted Igf1r gene".  
 RT Genomics 4:385-297(1997).  
 CC -!- FUNCTION: ACTIVATES THE CSBP2, P38 AND JNK MAP PATHWAYS, BUT NOT THE ERK PATHWAY. SPECIFICALLY PHOSPHORYLATES AND ACTIVATES MAP2K4 AND MAP2K6.  
 CC -!- SUBCELLULAR LOCATION: LOCALIZED IN PERNUCLEAR VESICULAR LIKE STRUCTURES, PROBABLY GOGLI-ASSOCIATED VESICLES.  
 CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A (SHOWN HERE) AND B; ARE PRODUCED BY ALTERNATIVE SPlicing.  
 CC -!- TISSUE SPECIFICITY: WIDELY EXPRESSED. HIGH EXPRESSION WAS FOUND IN SKELETAL MUSCLE, KIDNEY, TESTIS FOLLOWED BY HEART, BRAIN AND LUNG.  
 CC -!- EXPRESSION WAS FOUND IN SPLEEN.  
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC MAP KINASE KINASE KINASE SUBFAMILY.

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 -----  
 CC EMBL: 085607; AAC53126.1; -;  
 CC EMBL: 085608; AAC53127.1; -;  
 CC EMBL: 066240; AACU08286.1; -;  
 CC HSSP: P24941; IHCCL.  
 CC MGD: MGI:1346875; Map3k4.  
 DR InterPro: IPRO00220; Ser-thr-pkinase.  
 DR InterPro: IPRO00119; Euk\_pk kinase.  
 DR Pfam: PF00069; pk kinase; 1.  
 DR Prodrom; PD00001; Euk\_pk kinase; 1.  
 DR SMART; SM00240; S\_TKC; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 KW Transferase; Serine/threonine-protein kinase; ATP-binding;  
 KW Alternative splicing;  
 FT DOMAIN 117 1182 POLY-ALA.  
 FT DOMAIN 1332 13490 PROTEIN KINASE.  
 FT NP BIND 1338 13450 ATP (BY SIMILARITY).  
 FT BINDING 1361 1361 ATP (BY SIMILARITY).  
 FT ACT\_SITE 1452 1452 BY SIMILARITY.  
 FT VARSPLIC 1162 1213 MISSING (IN ISOFORM B).  
 FT CONFLICT 363 364 SL->NS (IN REF. 2).  
 FT CONFLICT 473 473 T->A (IN REF. 2).  
 SQ SEQUENCE 1597 AA; E84AAAE92D103A4 CRC64;  
 Query Match 6.1%; Score 475; DB 1; Length 1597;  
 Best Local Similarity 20.4%; Pred. No. 6.4e-13;  
 Matches 301; Conservative 211; Mismatches 576; Gaps 66;

Qy 169 TLKGHLKMDRPERMIREKLKATCPAWKHEW --ERRNRQGPVYVKPIVKGDSEEM 225  
 Db 363 SIQLAQKQDYERYAKQDFERVQACI L --- WLNITNDNQKLRLNGTVLGK -NUSDI 415  
 Qy 226 NHLAAE8PGEVOASRASPASGRSPSPONSRSPTVKE --- -SPGVRRKRVSPVPF 279  
 Db 416 GWPFEIP- --- SP --- RPSKGYEPEDEVETEVELRELESGTEESDEEPTP- 460  
 Qy 280 QSGRTPPRAPSPDGFSPYSP --- ET --- NRRVNVKYMARRLYLQQIGGNSFLIGG 331  
 Db 461 --- SPVPPELRSLTDITLDSSQCVSRK --- -LERLESEFDLSIGN 499  
 Qy 332 DSPDNKYRVTGPGONCSARGTCFTLIFYMLRQLEPSDPMWRLTKNFVEYESIFQK 391  
 Db 500 GTAD --- CGPE --- ASR --- HCLASIYRPFV --- -DKALKQMGILKLRL 536  
 Qy 392 YHS ----- RRSRRIKAPSRNTIQKFYSRMSNSHTLSSSENSTSSSENSTKDEEEOMC 443  
 Db 537 LHKLNGSLQRARVALVKDPRVERSDPFPWGSYVOLSGTPSS --- -EOKC 587  
 Qy 444 PICLGMIDEESLTYCEDG --- CRNLKH -HHCMSTIAWBECRNREPLICPL --- C 491  
 Db 588 SAVSWEELRAMLDPSPFEPATLVLCKVLLNTHEC1KLRLQE -RPAGEPLS1KQLVRQC 646  
 Qy 492 RSKWRSHDYFSHELSSPVDPSSSLRAAQQCTVQOQPLASRRNOESFNFTLHYSTQIPP 551  
 Db 647 KEVLK ----- STGNSGGSS ----- -STGNSGGSS ----- -STGNSGGSS -----  
 Qy 552 AKDLAEPWTOVF --- GMELVGLFISRWN --- VR - EMALRRLSHDVSGALL 596  
 Db 691 VYFDYMRSWIOMLQLPQASHSLKNLLEWFNTKEITHYIRGGEAQAKLFCDIAGML 750  
 Qy 597 LANGE ----- -GSSPGGSA 618  
 Db 751 KSTGSSFLESSGQESCAEWTSADDNGARDLRSVTEISALKELFHEARERASKALGFA 810  
 Qy 619 TGSQTSISDYYEACCS -VLSMKVADPVYKYYAALKTLRMLVYTCHSLAERIKL 676

Db	811	KMLRKDLEIAAEFVLSASARELDAKAKOYKVYQIPGLDBNLH--VVVP-DSIAEKKI	866	Schizosaccharomyces pombe (Fission yeast), Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Qy	677	QLLQPWVDTILVKCA--DANSRTSQLSISLSTLFLCKQAGELAVGREILKNGSIGGG	733	OC Schizosaccharomyces; OC Schizosaccharomyces; OC Schizosaccharomyces.
Db	867	--ILQ----LNATGKCSKEDDDVMDAFLLT -HGDIA-----	901	OX NCBI_TaxID=4996;
Qy	734	VDVVLNCILGNQTESNNWELLGRCLDRLLPAAEYPHIVSTDVSQAEPVE-IRYK	792	RN [1] SEQUENCE FROM N.A. RP MEDLINE=98026892; PubMed=93213959;
Db	902	--RDSDEGWGTWEARAVKI-----VQVEVYDTLRSM	931	RX RA Saitoima I., Mackie S., Fantes P.A.; RA "Multiple modes of activation of the stress-responsive MAP kinase pathway in fission yeast."; RT RL EMBO J. 16: 6162-6170(1997).
Qy	793	KLLSLTFAQOSIDNSHSMYKGKLSRRIYLSARAYTTVH-----VFSKLLMSSSS	845	RN [2] SEQUENCE FROM N.A. RP STRAIN=972;
Db	932	QVDNLVYVNE-----AHLV---LQRKAFOQSIEGLMTVRHEQTSSQPIAKGQQLK---	982	RC MEDLINE=21848401; PubMed=11859360;
Qy	846	STHETMRMRRLIMAIADEVEIAAQIQLGVEDILDGQDSF--LOASVPNNYLETTENSSP	902	RX RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., RA Sgourou S.J., Peat N., Hayles J., Baker S., Basham D., Bowman S., RA Brown S., Chillingworth T., Churcher C.M., RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jaggels K., RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J., RA Mooney P., Moule S., Murgail K., Murphy L., Niblett D., Odell C., RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbionitsch E., RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S., RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K., RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., RA Woodward J., Wolckert G., Aert R., Robben J., Gromponez B., RA Weltiens I., Vansteensels E., Rieger M., Schafer M., Mueller-Auer S., RA Gabel C., Fuchs M., Frizic C., Holzer E., Moestl D., Hilbert H., RA Borzym K., Langner I., Beck A., Lehrach H., Reinhardt R., Pohl T.M., RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B., RA Goiffau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., RA Lucas M., Rochet M., Gallard C., Talada V.A., Garzon A., Thode G., RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J., RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., RA Cerutti L., Lowe T., McCombie W.R., Pauslen I., Barrell B.G., Nurse P.; RA Shpakovski G.V., Ussery D., Poteashkin J., RT "The genome sequence of Schizosaccharomyces pombe."; RT Nature 415:871-880(2002).
Db	983	--NDALELCNRI----SDAIDRYDHMFTELEAEVESESAIQLQQYR	1024	RN [3] SEQUENCE OF 96-1401 FROM N.A. RP STRAIN=972;
Qy	903	ECTVHLKETG--KGCLCATKLASSDEDISERLASTSVGPSSSTTTTTEQPKPMYOT	958	RC MEDLINE=97282620; PubMed=9136929;
Db	1025	EAMIQGYNFGFFYHEKVRRLMSGEFRQKIGKDYISFAQKMNMYVLTKECEGRGTRPRWAT	1084	RX RA "The Mcs4 response regulator coordinately controls the stress- RT cycle through the Wki1-Wsi1-Spc1 kinase cascade."; RT RL Genes Dev. 11:1008-1022(1997).
Qy	959	KGRPHSQCLNSSLSPLSHSQMLPEALSTPSSSTPSAGATDVSXRLOGFLIPCRIPSAS	1018	RT RN [4] SEQUENCE OF 457-543 FROM N.A. RP STRAIN=972;
Db	1085	QDFDFLQATEPFASIPALPEDDLSQALMNECIGHVIG----KHF-----S	1126	RC MEDLINE=973311762; PubMed=9188094;
Db	1127	PV-----AIFRNSP-----RPPVYPRCHSDPPNPLHITPPEGFSTRS	1165	CC RA Saitoizaki K., Shiozaki M., Russell P.; CC "Mcs4 mitotic catastrophe suppressor regulates the fission yeast cell CC limited nutrition unlike Wki1, it is not activated by changes in CC the osmolarity of the extracellular environment. Activates the CC Wki1 MAP kinase kinase by phosphorylation." CC -1 SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. CC MAP KINASE KINASE SUBFAMILY.
Qy	1019	POTQERKSLOPFRNCPCPNKDSKLSPVFTQSRPLSSNIHRPKPSR--PTPGNTSKQG	1074	CC
Db	1166	VPSDARTHGSNTAAAAYRAAATTAAAGRPGPQGDSYPAK-----PNT-----	1209	CC
Qy	1130	SSIEDLLEASMSMSSDTTVTFKEAV----LSPKAENDDTY-KDDYNHNQKCKE--	1179	CC
Db	1210	-APDTRESSVPPENDRLASIAELOFLRSLSRSHSPTERDEPAYPRSDSSGSTRSWEIL	1267	CC
Qy	1180	KMABEEBALAZAMMASQDALIVPQLQVNGEDEIIIDPTEPLG--HTKAKQ	1235	CC
Db	1268	TLSQTQDSASKOGPIAQKSVRFLERRYREMRRKNTIGCVCDPKSYDNVMAYGLR-	1326	CC
Qy	1235	PYREDTEWLKGQQTIGLAFSSCYQADQVGTGTLMAYKQTVTRNTSSEQEVVEALREI	1295	CC
Db	1327	-KVTEFKQORGKNGKIGEQGKYKUTCISVDTGELMAKEIREFQN---DHKTKEADEL	1380	CC
Qy	1296	RAMSHLNHPNTIIMLGATCEKSYNLYTTEWMAGSYAHLLSRYGAKESVNTYBOLL	1355	CC
Db	1381	KIEFGIKIPNLYVFGVELHREMYIFMEYCDEGTLER-VSLGLG-LOEHVFLYRQITV	1438	CC
Qy	1356	GLSYLHENQOLIIRDYKQGANLIDSTGQRLIADEGAARLASKG-TGAGEFGQGOLLGIA	1414	CC
Db	1439	AINTVLHERRHGIVHLDIKGANTIFLTSSG-LIKLGDEGCSVTKLNQATMPGEV-NSTLGTAA	1496	CC
Qy	1415	FMAEVL--RGQYGRSCDWVGCAATEMACAKPPNAERHSNHALIFIASATTAP	1471	CC
Db	1497	YMAPEVITRAKGEHGRADIAWSLGCVVYTEMGTGRPHHEYBH--NFQIMXVGGMG-HKP	1553	CC
Qy	1472	SIPSHLSPGIRDYALRCLQDPRPSRELLKH	1505	CC
Db	1554	PIPERLSPGSKAFLSHCLESDPKIRWTASQLDH	1587	CC
RESULT 14				
ID	WIS4_SCHPO	STANDARD	PRT:	1401 AA.
AC	O14266;	PR07062; Q92384;		
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	MAP kinase kinase wisk1 (EC 2.7.1.-) (MAP kinase kinase kinase wak1) (MAP kinase kinase wak1)			
DE	WIS4 OR WAK1 OR WIKI OR SPAC9G1.02.			
GN				

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CC Homo sapiens (Human).  
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
CC OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
CC OC NCBI\_TAXID=9606;

CC RN SEQUENCE FROM N.A.  
CC RP MEDLINE=970750; PubMed=8940119;  
CC RX EMBL; Y18750; CAA69030\_1; ALT\_INIT.  
CC DR EMBL; Y11899; CAR7218\_1; .  
CC DR EMBL; U81511; AAB39762\_1; .  
CC HSSP; P24941; ICKP.  
CC DR InterPro; IPR007119; Euk\_pk kinase.  
CC DR InterPro; IPR002290; Ser-thr\_pk kinase.  
CC Pfam; PF00069; Pkinase; 1.  
CC DR ProDom; PD000001; Euk\_pk kinase; 1.  
CC SMART; SM00220; S\_TRC; 1.  
CC DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; FALSE\_NEG.  
CC DR PROSITE; PS00101; PROTEIN\_KINASE\_DOM; 1.  
CC DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
CC KW DOMAIN; 1306 PROTEIN KINASE.  
CC FT NP\_BIND 1043 1051 ATP (BY SIMILARITY);  
CC FT BINDING 1066 1066 ATP (BY SIMILARITY);  
CC FT ACT\_SITE 1161 1161 BY SIMILARITY.  
CC FT CONFLICT 484 485 RL -> SP (IN REF. 3).  
CC ET CONFlict 1346 1346 D -> V (IN REF. 1).  
CC SQ SEQUENCE 1401 AA; 160537 MW; 529A989D2B627F3D CRC64;

Query Match Score 5.5% Best Local Similarity 27.8%; Pred. No. 3e-11; Gaps 16; Matches 119; Conservative 86; Mismatches 162; Indels 61; Gaps 16;

CC 1103 NAVIPSDETVTPVEBKCRLDVNTEINSSLDL-EASMPSSDTTYTFKSEAVLSPEKA 1162  
Db 914 NNDTYKDDVHNQKCKEKEMAEEERALIAMMASQDALPIVPOLOVENGDIQQD 1222  
CC 1163 NDDEPLTFLKREK-----VGKSAFLI 1222  
CC 957 REST---EVSSSPRLTSFGDV-EEEALSQI---LQKETMLRIDEERNTTL---- 1004  
CC 1223 TPETLP-GHTAKQPRE-----DTEWIKGQIGLGFSSCYAQDYGTGL 1268  
Db 1005 --ERLAIGHVLDSSFRNRDFIKLASSFSNTIRHQGHVRSGMFQDVTGVMNETGDL 1062  
CC 1269 MAFQTYVTRATSEQEEVVALREPITRASHNPNIIMLGATEKSYNLFDEWMAG 1328  
Db 1063 LAVEKEKL--QDSRTRIRSTVQINHEMTVLERLNIFPVNVVYYGVHREKVYIIMEFQCG 1120  
CC 1329 GSVAHLLSKYGAFKESVINYTEQLLRLGSLYHENQTHRDVKGANLLDSTGQRRIAD 1388  
Db 1121 GSADLIAHGRTEDENTLVKVVQLEGAYIHSQHILHRDIKANILLDHRGM-IKYSD 1179  
CC 1389 FGAARIAASKTGTAEGEFQG----OLIGLTQFPEVLRQQYQ--RSQDWYSWGCAII 1440  
Db 1180 FGSALEYSPPDPEVRYEDIQPELQHLAGIPMVAPELIIGTKDFGAMDIWUGCVIL 1239  
CC 1441 ENACAKPPWNAEKHSNLALIFKIASATTAPSISPH--LSPGLRROYALRCLELQFQDRPP 1498  
Db 1240 EATGTSIPIWS--EMDNIEWAIMYHVAAMHT-PSIPQNEKISSLARDIEQCFFERDEQRPR 1296  
CC 1499 SRELIKHP 1506  
Db 1297 AVDLLTHP 1304

Query Match Score 5.5% Best Local Similarity 36.6%; Pred. No. 4e-11; Gaps 21; Gaps 7;

CC RESULT 15  
ID M315\_HUMAN STANDARD; PRT; 1374 AA.  
AC Q96833; Q99461; 39, Created)  
DT 30-MAY-2000 (Ref. 39, Last sequence update)  
DT 30-MAY-2000 (Ref. 39, Last annotation update)  
DE Mitogen-activated protein kinase kinase kinase 5 (MEK 5) (Apoptosis signal-regulating kinase 1) (ASK-1).  
DE (MAPK/ERK kinase kinase 5) (MEK kinase 5) (MEKK 5) (Apoptosis signal-regulating kinase 1) (ASK-1).  
DE MAP3K5 OR MAPKK5 OR MERK5 OR ASKL.

Qy	1249	IGLGAFSSCYQAQDVGTLGMLAVKQTVYRNTSEQQVEALRETRMMSHLNHNPNTIR	1.308
Db	686	LKGKTYGIVTYAGRDLNSQRYIAKEI-----PERSRSQPLHEFALHKHLKHKNVQ	7.39
Qy	1309	MLGATCEKSNNYLFEWAGGSVAHL-L-SKYGAFK - BSVVINYTEQQLRGSLYHLHENQI	1.365
Db	740	YLGSSENGFIKIMEQVGGSLSALLSKWGLPKDNENOTIGYTQKILEGKLHYHNQI	7.99
Qy	1366	IHDYRGANLJIDSTGQRRIADFGAARLASKRTGAGEFGQOLGTIAFMADPEVL---	1.421
Db	800	VHRDKGDNLYINTSGVLUKISDGTSKLA-----GINPCTERFTGTLQYMAPEITDKGP	8.55
Qy	1422	RGQQGRSGWSYCACTEMACAKPPWAEKISHNLALIFKA	1.481
Db	856	RG-YGKAADIWLWLGCTITEMATGKPF--YELGEPOAMFKYGMFKYHPEIPESMSSEA	9.11
Qy	1482	RDVALRCLELQPDRPSSRL	1.503
Db	912	KAFTKCFKCBEDPDKACANDI	9.33

Search completed: December 20, 2002, 16:21:22  
Job time : 34 secs